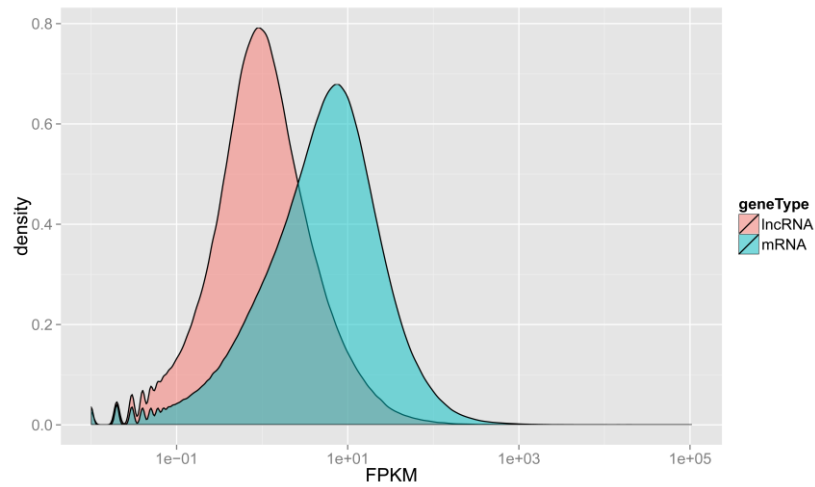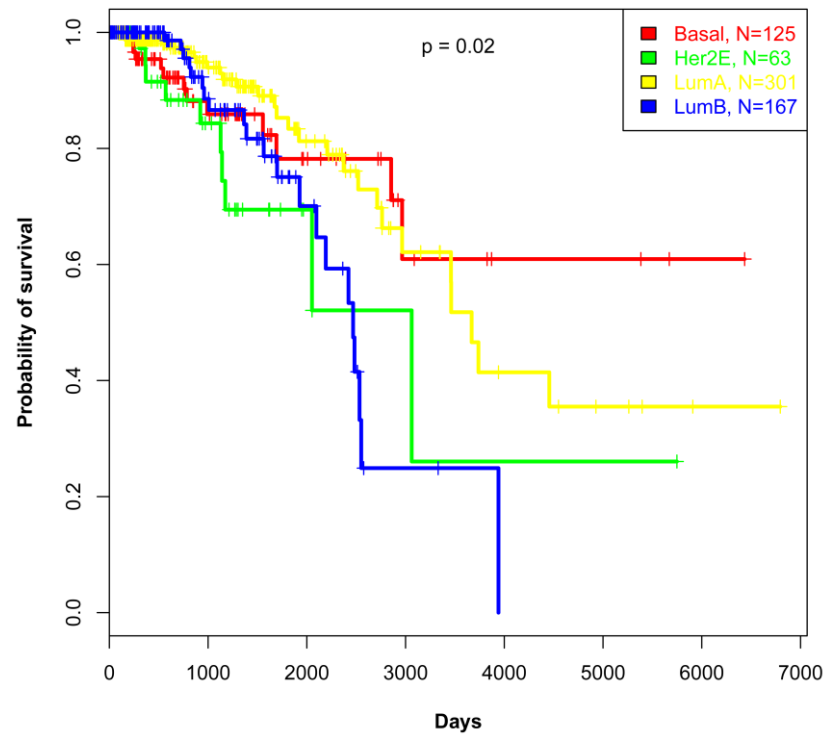# Comprehensive analysis of long non-coding RNAs in human breast cancer clinical subtypes
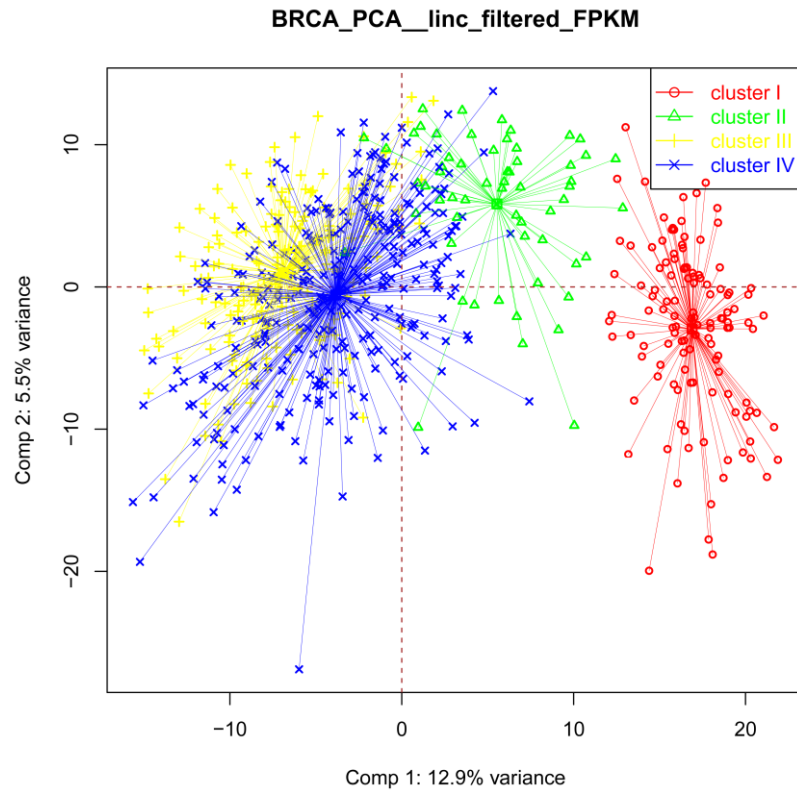
**Supplementary Material**

Supplemental Figure S1: FPKM density plots of mRNAs and lncRNAs expression in the breast

dataset of The Cancer Genome Atlas (TCGA)

Supplemental Figure S2: Kaplan-Meier curves for overall survival time in patients with breast cancer according to PAM50 classification.

BRCA_PCA__linc_filtered_FPKM

Supplemental Figure S3: Principal component analysis of lncRNA datasets. Results were

projected on the first 3 components, and show 4 main sample clusters highlighted in different

colors. BIC is Bayesian information criterion.
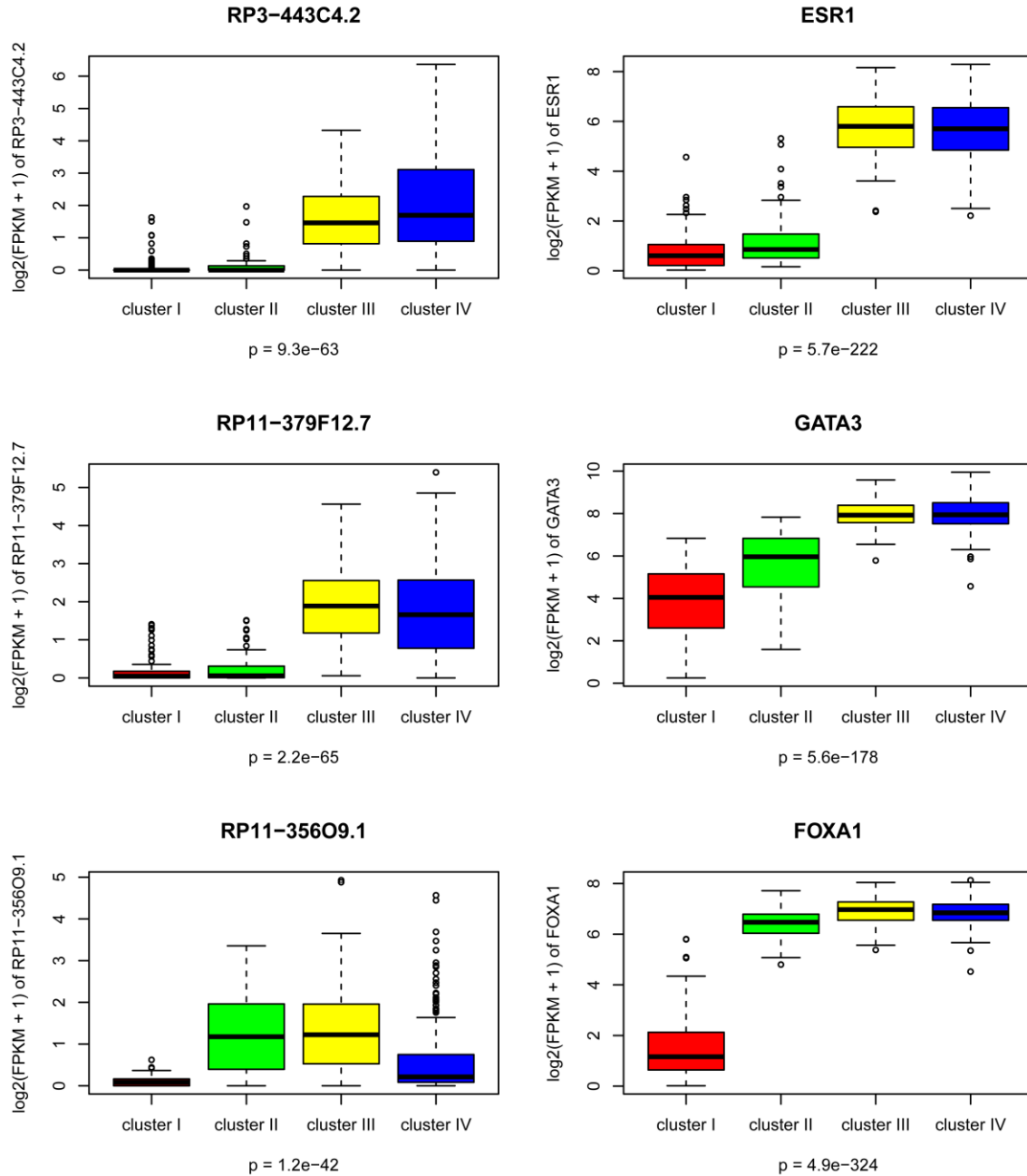
Supplemental Figure S4: Box-plots for the expression levels of *ESR1, GATA3* and *FOXA1* as well as their neighboring lncRNAs showing their coordinated expression in luminal breast cancer but not in basal-like breast cancer as the high expression of these genes is characteristic in luminal breast cancer.
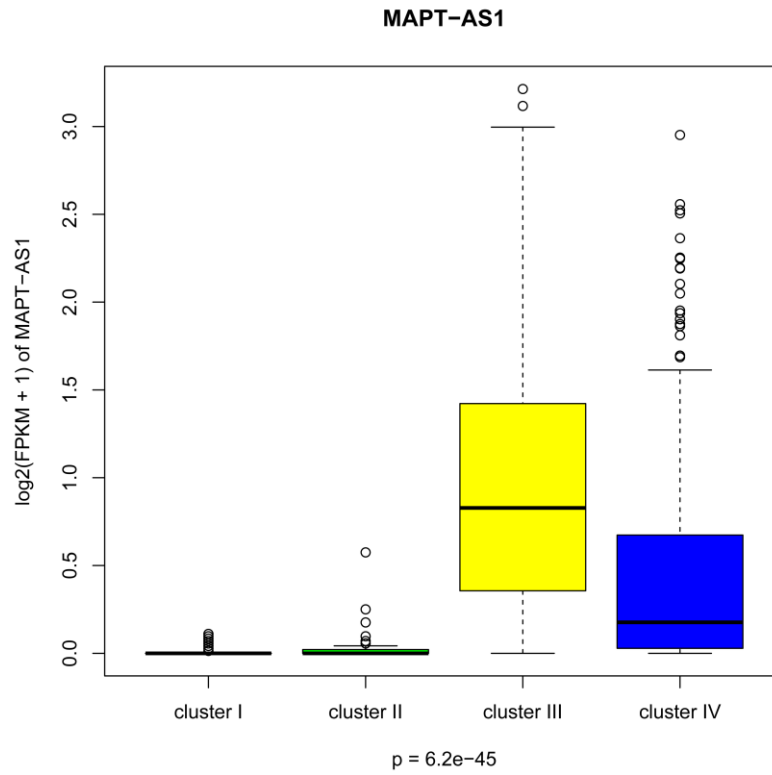
Supplemental Figure S5: Boxplot for expression levels of MAPT-AS in the 4 subgroups of

lncRNA classification.